Hierarchical Optimization for Procedural Effectiveness in Diagnosing Mutations That Relate to Disease

Field of Invention

This invention relates to computer readable mediums, systems and methods for determining an optimal test order for diagnosing mutations that relate to a disease.

Background

For certain diseases linked to autosomal dominant inheritance of genetic mutations, doctors are now able to improve medical treatment for affected people, even before clinical presentation of symptoms, due to molecular diagnosis of the heritable mutation. Some diseases that result from such heritable mutations are hereditary breast and ovarian cancer, hereditary hemorrhagic telangiectasia, cystic fibrosis, colorectal cancer and retinoblastoma.

For example, molecular diagnosis requires a comparison of patient DNA to "wild type" DNA accepted by a consensus of experts as normal. Some general classes of mutations that cause disease include deletion of all or part of a critical gene, insertions and duplications of isolated portions of DNA, and hypermethylation of gene promoter regions. In some diseases, certain genetic mutations are found to recur in the DNA of many patients, the same type of mutations at the same locations in DNA, across many individuals.

For example, in both Duchenne Muscular Dystrophy and Becker Muscular Dystrophy, mutations cluster in two recombination "hot spots" [Den Dunnen et al 1989]. Similarly, the most common genetic defect that causes cystic fibrosis (ΔF508) accounts for about 30-80% of mutant alleles depending on the ethnic group [CF Genotype-Phenotype Consortium1993].